AMENDMENTS TO THE CLAIMS

1. (Cancelled).

2. (Currently Amended) A method according to claim 25~~1~~, further comprising amplification of the interacted nucleic acids and quantification of the amplification product.

3. (Currently Amended) A method according to claim 25~~1~~, wherein the binding moiety of the proximity probes is selected from the group consisting of proteins, peptides, carbohydrates, nucleic acids and combinations thereof.

4. (Currently Amended) A method according to claim 25~~-1~~, wherein the one or more analytes are selected from the group consisting of proteins, protein aggregates, prions and nucleic acids.

5. (Currently Amended) A method according to claim 25~~1~~, wherein the binding sites for the binding moieties of the proximity probes are on one and the same analyte, or on two close analytes.

6. (Currently Amended) A method according to claim 25~~1~~, wherein the binding moieties are antibodies and said antibodies each bind to the one or more analytes via a further antibody having binding specificity for the one or more analytes analyte(s), and wherein the binding moieties are directed against the Fc portion of the further antibody.

7. (Currently Amended) A method according to claim 25~~1~~, wherein the interaction of said nucleic acids coupled to the binding moieties is through hybridisation to a common splint template and ligation of the nucleic acid ends.

8-12. (Cancelled).

13. (Currently Amended) A method according to claim 25~~1~~ for screening for ligand-receptor interaction antagonists in a high throughput screening procedure, wherein a drug candidate molecule is screened for ability to disrupt proximity between the proximity probes.

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14. (Currently Amended) A method according to claim 25~~1~~, wherein the first proximity probe is comprised of purified analyte coupled to an oligonucleotide and the second proximity probe is comprised of a binding moiety specific for the analyte with a coupled oligonucleotide capable of interacting with the first proximity probe .

15. (Currently Amended) A method according to claim 25~~13~~ wherein the drug candidate molecule is a biomolecule derived from a library of potential ligands to one of the binding sites involved in the formation of the proximity between the proximity probes .

16. (Cancelled).

17. (Currently Amended) A method according to

claim 25~~1~~, comprising using said method for the detection of infectious agents.

18. (Previously Amended) A method according to claim 17, wherein the infectious agents are detected in food for humans and animals.

19. (Currently Amended) The method according to claim 25~~1~~, further comprising quantifying the interaction of the analytes in solution.

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20. (Previously Added) A method according to claim 19, further comprising amplification of the interacted nucleic acids and quantification of the amplification product.

21. (Previously Added) A method according to claim 14, wherein the presence of an analyte in a sample is detected as a decrease in signal.

22. (Currently Amended) A method according to claim 25~~1~~, wherein said two or more proximity probes comprise a first said proximity probe with a 3′ free nucleic acid (A), a second said proximity probe with a 5′ free nucleic acid (B), and a third said proximity probe with both 3′ and 5′ free nucleic acids (C), and wherein the 3′ end of A interacts with the 5′ end of C and the 3′ end of C interacts with the 5′ end of B.

23. (Previously Added) A method according to claim 3, wherein the proteins are selected from the group consisting of monoclonal antibodies, polyclonal antibodies, lectins, soluble cell surface receptors, combinatorially derived proteins from phage display, and combinatorially derived proteins from ribosome display.

24. (Previously Added) The method of claim 3, wherein the nucleic acids are aptamers.

25. (Currently Amended) A method for detecting one or more analytes in solution, comprising:

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a) binding ~~of~~ two or more proximity probes to a respective binding site on said one or more analytes not immobilized on a solid support,

wherein the proximity probes comprise ~~are comprised of~~ a binding moiety with affinity for said one or more analytes and nucleic acids acting as a reactive functionality coupled thereto;

b) allowing the binding moiety to bind to the one or more analytes other than by Watson-Crick base pairing and allowing the nucleic acids to interact with each other if they are in close proximity to each other; and

c) detecting the degree of interaction between the nucleic acids.